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09/776, 705
 DIALCG
 file 12054
 1/28/03

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3	BRS	14	BRANDON-RHONDA-C	USPAT; US-PGPUB; EPO; JPO; DERWENT
4	BRS	38	MERKULOV-GENNADY-V	USPAT; US-PGPUB; EPO; JPO; DERWENT
5	BRS	106	KETCHUM-KAREN-A	USPAT; US-PGPUB; EPO; JPO; DERWENT
6	BRS	9	DIFRANCESCO-VALENTINA	USPAT; US-PGPUB; EPO; JPO; DERWENT
7	BRS	247	BEASLEY-ELLEN-M	USPAT; US-PGPUB; EPO; JPO; DERWENT
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07/776, 705

LOCUS AC005854 37921 bp DNA linear PER 20-MAR-1999
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 ACCESSION AC005854
 VERSION AC005854.2 GI:4454968
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 37921)
 AUTHORS Montgomery, P.T., Lau, S.T. and Fucherlapati, R.
 TITLE High Throughput Sequencing of Human Chromosome 12
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 37921)
 AUTHORS Montgomery, P.T., Lau, S.T. and Fucherlapati, R.
 TITLE Direct Submission
 JOURNAL Submitted (23-SEP-1998) Department of Molecular Genetics, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
 REFERENCE 3 (bases 1 to 37921)
 AUTHORS Montgomery, P.T.
 TITLE Direct Submission
 JOURNAL Submitted (21-MAR-1999) Molecular Genetics, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
 COMMENT On Mar 20, 1999 this sequence version replaced gi:3785953.
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[illegible]

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3761 cattaaagct acatttttca gttcttaaat gttctttaa taccctctag gagtacaaat
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3841 aactttgttc taaaataat ccttaaata aatgttcaaa ttaagaaata aaggtaagac
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3891 atataataa ctcaactat tttaacagct ctatttgaat tpttctctt tctttttatt
3901 caattgtcta atttattat aaacttaaaa ttatctgaa agaaaacttg caattaggac
3911 ctggttaaat aattctatg ttgtcaatta tacttaattg atcatttcta caattaggaa
3921 acaactttat caactctaa ttcttaaaaa ttcttattt taattataaa acacacaca
3931 caatcaaat aagaaagtaa caattttt aactctgaa atattctatg aaaaacagct
3941 ttttcaaat tatttattaa ctcttgcga ggttctctg attcttttg aatggcagac
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3961 ctgagagga agaaaatag ccaatcaaaa ccaacacac ccccaacac cctctctgt
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3991 caactcaaat acaacttcaa agtttttagt tggthgtgt cattctctat caagtttta
4001 ctgaggtgct tgcctgtcga atcagaaat attcgtttt aaaaacatt tgaattgaa
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4021 tgaactctc cagaaatac tpaactata ctgaaaggt tattttctt tgaattgtg
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36961 gatggtgtgg aggtggtggt ggaggtggag gtgggtacaa ggaggccagt aggaaggttg
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37141 tttttttatc actttcacta gtcacaatg ctatgaattt taagtgtca ttttatgaaa
37201 aacaagaact agcaataaaa tcttcatttt cttacatag agaaagagaa cgtatggtga
37261 taattcatcc atttcaaac ccgtttcatt aatctatgac tatcacttc aaatagtgt
37321 gagaagggtc tagaatgtac atcccaatgt aatgttatct attgaaaaa caagaatggt
37381 ggtcctaaaat acagtgtatc agattatacc tgtacattga ataagaaat ttcttataca
37441 tattttaaatt cattgattat atggtttcaa atttctacct ccaacaatga ccttaagag
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37561 tcatggtatt ttgcaacgac agtgggagag ataaactgtt gttctcgtca tgactatacc
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37861 ttgtatttat gatgccttat tctccaagaa gttacctttt accgtagatt cataaaactca
37921 a
```

//

LOCUS AC001014 167939 bp DNA linear PRI 20-AUG-2000
 DEFINITION Homo sapiens 12 BAC RPC111-66E20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.

AC001014
 VERSION AC001014.0 GI:5411133
 KEYWORDS BAC

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 167939)
 AUTHORS Wang, J., Arenson, A.L., Bouck, J., Burac, S., Chen, Z., Ding, Y.,
 Fernald, S., Furuta, J., Forcum, C., Garcia, C., Gorrell, J.H.,
 Hsu, J.L., Hernandez, J., Kasar, A., Jackson, L., Kneitz, S.,
 Kunkel, N., Lai, S., Leal, E., Lee, H., Licata, D., Lu, W.,
 Liang, D., Lu, T., Marand, H., Martinen, C., Marschner, S., Miller, A.,
 Montgomery, K., Ngai, L., Pappas, L.R., Parish, E.J., Perez, L.,
 Rasmussen, S., Rhee, S., Scherer, S.F., Shen, K., Shim, C., Simon, M.,
 Si, J., Williamson, A., Worley, K.C., Khang, A.M., Yang, R., Yu, W.,
 Zeng, X., Zuchowicz, S., Nelson, D. and Sikhs, R.A.
 TITLE Direct Submission

JOURNAL Submitted (10-JUL-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 REFERENCE 2 (bases 1 to 167939)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 167939)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (17-SEP-1999) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE 4 (bases 1 to 167939)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAR-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE 5 (bases 1 to 167939)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-AUG-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

REFERENCE 6 (bases 1 to 167939)
 AUTHORS Worley, K.C.
 TITLE Direct Submission
 JOURNAL Submitted (30-AUG-2000) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA

COMMENT on Sep 1, 1999 this sequence version replaced gi:5411133.
 CHROMALPAC: <http://www.ngsc.bcm.tmc.edu> or email
 pc-nhgsc@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
 entire insert of this clone. Overlapping regions of clones are only
 sequenced and submitted once, so the sequence for the remainder of
 the insert may be found in the record for the adjacent clones.
 Overlapping clones are noted at the beginning and end of the
 Features listing.

ANNOTATION OF FEATURES:
 CTSS are identified using cPCR (Genome Res. 7:541-550) searches

of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for human and mouse sequences.

Genes and logic of sequence similarity are identified by BLAST (Nuc. Acids Res. 21:3239-3402) similarity (expect < 1e-04) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - (estimated error rate less than 1 per 10,000 bases. Reports of 1 worst quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://ge.com.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----

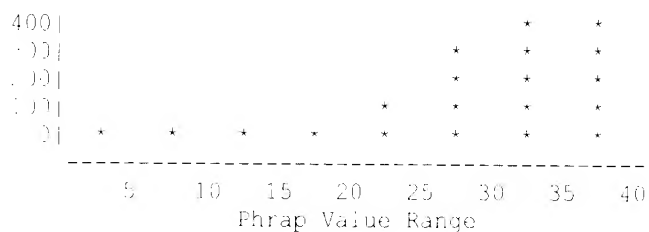
Contig length:	187389
Phrap values in estimate:	187443
Average error rate (ECM-Phrap estimate):	6.73211e-05
Fraction of Phrap values less than 40 :	0.0031645
Number of consensus changing edits:	16
Number of N's in consensus :	0

----- Consensus changing edits -----

Position	Original+Context	Edited+Context
50678	gctctaggta(n)agccttttagt	gctctaggta(g)agccttttagt
70961	taaaaacaaa(n)acaaaactcc	taaaaacaaa(a)acaaaactcc
121825	tatattaaaa(n)tntatacaaa	tatattaaaa(a)tatatacaaaa
121827	tattaaaant(n)tntacaaaata	tattaaaant(a)tacacaaaata
121829	ttaaaantnt(n)tacaaaatata	ttaaaantat(a)tacaaaatata
121831	ataaaaattg(n)gtatatataa	ataaaaattg(t)gtatatataa
121835	aacatatatg(n)atatattatt	aacatatatg(t)atatattatt
121837	ctttccgggg(n)aggagggaag	ctttccgggg(a)aggagggaag
121839	tatcttggtta(n)tcttttagtgc	tatcttggtta(c)tcttttagtgc
121841	tcttttagtgc(n)attaagtaat	tcttttagtgc(t)attaagtaat
121843	tttagtgcta(n)taagtaatga	tttagtgcta(t)taagtaatga
121845	taataggggg(n)aattatttgt	taataggggg(a)aattatttgt
121847	ctctgtcacc(n)aggctggagt	ctctgtcacc(c)aggctggagt
121849	atctttaaant(n)gtagctgctc	atctttaaant(c)gtagctgctc
121851	aacattgtta(n)aatatatat	aacattgtta(a)aatatatat
121853	cattgttana(n)atatatatat	cattgttana(a)atatatatat

----- Distribution of Quality < 40 Bases -----

1000	*	*
900	*	*
800	*	*
# 700	*	*
bases 600	*	*
500	*	*



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Version: 1.01  qxfg.
FEATURES             Location/Qualifiers
     source            1..167539
                     organism="Homo sapiens"
                     db_xref="taxon:9606"
                     chromosome="12"
                     clone="BF11-66E20"
     misc_feature      1..2051
                     note="overlaps bases 101954..104000 of clone AC008035"
                     function="clone overlap"
     repeat_region     complement(130..339)
                     rpt_family="MER5A"
     misc_feature      339..1117
                     note="Region: Similar to clone oz01c01.x1 Homo sapiens
                     CCA, A1276326."
     repeat_region     1..1194
                     rpt_family="T3ta"
     repeat_region     1194..1968
                     rpt_family="L3Aa"
     repeat_region     1968..11405
                     rpt_family="AT-rich"
     repeat_region     11405..1612
                     rpt_family="AT-rich"
     repeat_region     1612..2294
                     rpt_family="AluSp"
     repeat_region     2294..3392
                     rpt_family="(CAA)n"
     repeat_region     complement(3592..4002)
                     rpt_family="L1MC1"
     repeat_region     complement(4057..4201)
                     rpt_family="L1M4"
     repeat_region     complement(4217..6422)
                     rpt_family="L1MC1"
     repeat_region     6426..6705
                     rpt_family="L1M4"
     repeat_region     complement(6711..7335)
                     rpt_family="L1M4"
     repeat_region     7335..14306
                     rpt_family="L1PA14"
     repeat_region     14307..14930
                     rpt_family="L1PA14"
     repeat_region     complement(14933..15220)
                     rpt_family="L1MEc"
     repeat_region     complement(15231..15547)
                     rpt_family="AluSx"
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     repeat_region     15569..15642
                     rpt_family="(TTAA)n"
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                     rpt_family="L1MEc"
     repeat_region     complement(16065..16356)

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repeat_region      rpt_family="AluSk"
                    complement(16257..17228)
                    rpt_family="L1MEc"
repeat_region      complement(17400..17565)
                    rpt_family="L1MEc"
repeat_region      complement(17517..17593)
                    rpt_family="L1MCa"
repeat_region      complement(18110..18383)
                    rpt_family="L1HE1C"
repeat_region      complement(18381..18387)
                    rpt_family="L1HE1C-internal"
repeat_region      complement(19033..20140)
                    rpt_family="L1HE1C"
repeat_region      1161..10409
                    rpt_family="AluY"
repeat_region      11991..10705
                    rpt_family="L1MTB"
repeat_region      complement(20747..20825)
                    rpt_family="L1PA1"
repeat_region      complement(20747..20837)
                    rpt_family="L1MCa"
repeat_region      1161..1181
                    rpt_family="AT-rich"
misc_feature        1117..1180
                    note="Region: Uniprot cluster similar to AA310834 and
                    20575."
repeat_region      complement(1310..13666)
                    rpt_family="L1"
repeat_region      13704..13930
                    rpt_family="L1S"
repeat_region      14001..14374
                    rpt_family="A-rich"
repeat_region      14376..14377
                    rpt_family="L1GGGA-rich"
repeat_region      complement(14415..15119)
                    rpt_family="AluSg"
repeat_region      15118..15511
                    rpt_family="L1"
repeat_region      complement(15516..15520)
                    rpt_family="L1T816A1"
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                    rpt_family="L1"
repeat_region      complement(16007..16159)
                    rpt_family="L1"
repeat_region      16159..16164
                    rpt_family="(L1)n"
repeat_region      complement(17451..17339)
                    rpt_family="AluJk"
repeat_region      1710..18103
                    rpt_family="L1S"
repeat_region      18189..19317
                    rpt_family="AT-rich"
repeat_region      complement(19608..19609)
                    rpt_family="L1H94"
repeat_region      complement(19714..19719)
                    rpt_family="L1H"
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repeat_region      complement(19917..19448)
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repeat_region      complement(19577..19563)
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repeat_region      complement(19703..19707)

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                    7478..3881
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                    complement(39021..39370)
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                    43846..43848
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                    complement(43851..43996)
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repeat_region 5547..5547
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repeat_region 55265..56335
/rpt_family="MLT1H"
repeat_region complement(55869..58747)
/rpt_family="MLT1F1"
repeat_region complement(58791..59249)
/rpt_family="MLT1F1"
repeat_region 55763..56335
/rpt_family="MLT1H"
misc_feature 55965..56395
/Note="Region: Similar to clone AA828609 and AA993965."
repeat_region 55965..56344
/rpt_family="(A)n"
repeat_region complement(56090..57016)
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repeat_region complement(56051..57327)
/rpt_family="MIF"
repeat_region complement(56117..57367)
/rpt_family="MER"
repeat_region complement(56417..57515)
/rpt_family="L2"
repeat_region 56416..57367
/rpt_family="(TTTTC)n"
repeat_region complement(57327..57236)
/rpt_family="L1PA2"
repeat_region 57236..57236
/rpt_family="L1PA2"
repeat_region 57236..57236

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repeat_region      rpt_family="MIR"
                    complement(79108..79323)
                    rpt_family="L1M4"
repeat_region      complement(79323..79538)
                    rpt_family="(TGT)n"
repeat_region      complement(79538..80000)
                    rpt_family="AluSx"
repeat_region      complement(80000..80215)
                    rpt_family="(TAAA)n"
repeat_region      complement(80215..80430)
                    rpt_family="L1KA4A"
repeat_region      complement(80430..80645)
                    rpt_family="L1KA4A"
repeat_region      complement(80645..80860)
                    rpt_family="L1KEc"
repeat_region      complement(80860..81075)
                    rpt_family="AluJb"
repeat_region      complement(81075..81290)
                    rpt_family="AluY"
repeat_region      complement(81290..81505)
                    rpt_family="(GTTT)n"
repeat_region      complement(81505..81720)
                    rpt_family="AluY"
repeat_region      complement(81720..81935)
                    rpt_family="L1PA1"
repeat_region      complement(81935..82150)
                    rpt_family="L1ND3"
repeat_region      complement(82150..82365)
                    rpt_family="L1PA12"
repeat_region      complement(82365..82580)
                    rpt_family="(TGT)n"
repeat_region      complement(82580..82795)
                    rpt_family="L1PA15"
repeat_region      complement(82795..83010)
                    rpt_family="MSTB-internal"
repeat_region      complement(83010..83225)
                    rpt_family="MSTB"
repeat_region      complement(83225..83440)
                    rpt_family="L1MEc"
repeat_region      complement(83440..83655)
                    rpt_family="L1P4"
repeat_region      complement(83655..83870)
                    rpt_family="THB1B"
repeat_region      complement(83870..84085)
                    rpt_family="L1P4"
repeat_region      complement(84085..84300)
                    rpt_family="AT_rich"
repeat_region      complement(84300..84515)
                    rpt_family="FLAM_A"
repeat_region      complement(84515..84730)
                    rpt_family="HEFVL"
repeat_region      complement(84730..84945)
                    rpt_family="MLT1H"
repeat_region      complement(84945..85160)
                    rpt_family="MLT1H"
repeat_region      complement(85160..85375)
                    rpt_family="AT_rich"
repeat_region      complement(85375..85590)
                    rpt_family="AT_rich"
repeat_region      complement(85590..85805)
                    rpt_family="L1PA16"
repeat_region      complement(85805..86020)
                    rpt_family="MIR"
misc_feature        complement(86020..86235)
                    note="Region: Similar to clone ni45c09.s1 Homo sapiens

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cDNA, AA508410."
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  /size:12..32444
  /rpt_family:"(CAAAA)n"
  /size:97..92422
  /rpt_family:"MIR"
  /complement:9392..94056)
  /rpt_family:"MEF94"
  /size:112..94412
  /rpt_family:"AT rich"
  /complement:9463..94997)
  /rpt_family:"HA11"
  /size:61..95440
  /rpt_family:"AluSc"
  /size:14..96112
  /rpt_family:"L2"
  /size:14..96664
  /rpt_family:"AT rich"
  /complement:9673..97571
  /rpt_family:"LINA7"
  /size:14..98364
  /rpt_family:"LINA7"
  /complement:98112..98561)
  /rpt_family:"MLT2A"
  /complement:98366..10253)
  /rpt_family:"HEFVL"
  /size:31..101664
  /rpt_family:"AluX"
  /size:106..101776
  /rpt_family:"L1FA4"
  /size:37..103064
  /rpt_family:"AluX"
  /complement:103064..104736)
  /rpt_family:"HEFVL"
  /complement:104737..105178)
  /rpt_family:"MLT2A"
  /complement:105184..105425)
  /rpt_family:"MIF"
  /size:30..105807
  /rpt_family:"L1FA15-16"
  /size:92..107482
  /rpt_family:"L1F6"
  /complement:107486..107679)
  /rpt_family:"AluSg/x"
  /size:53..108119
  /rpt_family:"L1F4"
  /size:26..114061
  /rpt_family:"L1FA6"
  /size:91..113122
  /standard_name:"G19948"
  /xref="dbSTS:2826"
  /size:376..113124
  /rpt_family:"L1F4"
  /size:39..117501
  /rpt_family:"AluSg"
  /size:53..117513
  /rpt_family:"L1F6"
  /size:94..118116
  /rpt_family:"L1FA14"
  /size:36..118368
  /rpt_family:"L1FA4"
  /size:11..120734
  /rpt_family:"L1FA14"
  /size:36..121366

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repeat_region      (rpt_family="L1PA16"
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rpt_family="AT-rich"
misc_feature      101755..1..1847
function: "Low coverage."
repeat_region      101755..1..1946
rpt_family="ITAn"
repeat_region      101806..1..2001
rpt_family="GTAAn"
repeat_region      101855..1..2107
rpt_family="LINE"
repeat_region      101944..1..2161
rpt_family="L1HA9"
repeat_region      complement(101975..124277)
rpt_family="AATAn"
repeat_region      102037..1..2434
rpt_family="AT-rich"
repeat_region      102419..1..2514
rpt_family="LINE"
repeat_region      102506..1..2571
rpt_family="L1H83"
repeat_region      complement(102567..126114)
rpt_family="LINE"
repeat_region      102673..1..2633
rpt_family="L1PA2"
repeat_region      complement(102751..127378)
rpt_family="L1"
repeat_region      102801..1..2613
rpt_family="LINE"
repeat_region      102833..1..2904
rpt_family="HBB44A"
repeat_region      complement(102841..138237)
rpt_family="L1"
repeat_region      102843..138300
rpt_family="TDSAn"
repeat_region      complement(102897..138704)
rpt_family="MLT1A2"
repeat_region      102905..1..3006
rpt_family="THE1B"
repeat_region      102970..138624
rpt_family="THE1B-internal"
repeat_region      103005..138988
rpt_family="THE1B"
repeat_region      complement(103038..131051)
rpt_family="MLT1A2"
repeat_region      complement(103135..131469)
rpt_family="A13x"
repeat_region      complement(103173..132035)
rpt_family="A13Y"
repeat_region      complement(103233..132378)
rpt_family="LINE"
repeat_region      complement(103274..132679)
rpt_family="A13Y"
repeat_region      complement(103680..133819)
rpt_family="LINE"
repeat_region      complement(104111..134526)
rpt_family="HST3"
repeat_region      104546..134879
rpt_family="LINE"
misc_feature      104635..134619
function: "Region: 'Unigene cluster similar to H55836,
A1376648, AA70592.'"
gene              104703..134734
function: "H.sapiens gene for early lymphocyte activation
antigen CD69, exon 4"

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repeat_region 138161..138197
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repeat_region 138198..138242
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repeat_region complement(138243..138445)
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repeat_region 138446..138489
                /rpt_family="T18"
repeat_region complement(138490..140574)
                /rpt_family="T18B4"
repeat_region 140575..140618
                /rpt_family="T18B7A"
repeat_region 140619..140662
                /rpt_family="AT-rich"
repeat_region 140663..140706
                /rpt_family="L2"
misc_feature 140707..140750
                /note="Region: Similar to clone zille12.s1 Homo sapiens
                cDNA, AA68136.1."
repeat_region complement(140751..151163)
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repeat_region 151164..151207
                /rpt_family="T18A8"
repeat_region complement(151208..151712)
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repeat_region 151713..151856
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repeat_region 151857..151900
                /rpt_family="AT-rich"
repeat_region 151901..151944
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repeat_region complement(151945..151694)
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repeat_region 151695..151838
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repeat_region 151839..151982
                /rpt_family="(T)n"
repeat_region complement(151983..152377)
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repeat_region 152378..152521
                /rpt_family="AluSq"
repeat_region complement(152522..152643)
                /rpt_family="L2"
repeat_region complement(152644..152613)
                /rpt_family="L2"
repeat_region 152614..152657
                /rpt_family="T18"
misc_feature 152658..152701
                /note="overlaps bases 1..2006 of clone AC080136"
                /function="clone overlap"
repeat_region complement(152702..152711)
                /rpt_family="HALL"
repeat_region complement(152712..152721)
                /rpt_family="HALL"
misc_feature 152722..152731
                /note="Region: Similar to clone oy88b03.x1 Homo sapiens
                cDNA, AF075114.1."

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BASE COUNT 53499 a 31963 c 33412 g 50973 t

ORIGIN

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121 aaatgattac tctctctctc ctgttcagg gtctctcaaac attggaatgc atcaaaaaaa
181 tctgaagagt tctctcaaac atagatttct gatttccaac tccagaattt gtgattcaat

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241 agatccagag tagatccaa gaatttgcgc ttctaacaca tttagaggtg atgctgatgc
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51

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